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Modeling Microbial Responses in Food
Robin C. McKellar and Xuewen Lu

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CRC PRESS
Boca Raton London New York Washington, D.C.

Library of Congress Cataloging-in-Publication Data

Modeling microbial responses in foods / edited by Robin C. McKellar and Xuewen Lu.
p. cm. — (CRC series in contemporary food science)
Includes bibliographical references and index.
ISBN 0-8493-1237-X (alk. paper)
1. Food—Microbiology. I. McKellar, Robin C., 1949–II. Lu, Xuewen. III. Series.

QR115.M575 2003
664′.001′579—dc22 2003055715

Direct all inquiries to CRC Press LLC, 2000 N.W. Corporate Blvd., Boca Raton, Florida 33431.

Visit the CRC Press Web site at www.crcpress.com

International Standard Book Number 0-8493-1237-X
Library of Congress Card Number 2003055715
Printed in the United States of America 1 2 3 4 5 6 7 8 9 0
Printed on acid-free paper

Preface

The field of food microbiology is a broad one, encompassing the study of microorganisms that have both beneficial and deleterious effects on the quality and safety of raw and processed foods. The microbiologist's primary objective is to identify and quantify food-borne microorganisms; however, the inherent inaccuracies in the enumeration process and the natural variation found in all bacterial populations complicate the microbiologist's job. Accumulating sufficient data on the behavior of microorganisms in foods requires an extensive amount of work and is costly. In addition, while data can describe a microorganism's response in food, they provide little insight into the relationship between physiological processes and growth or survival. One way this link can be made is through the use of mathematical models.

In its simplest form, a mathematical model is a simple mathematical description of a process. Models have been used extensively in all scientific disciplines. They were first used in food microbiology in the early 20th century to describe the inactivation kinetics of food-borne pathogens during thermal processing of foods. Since then, with the advent of personal computers and more powerful statistical software packages, the use of modeling in food microbiology has grown to the point of being recognized as a distinct discipline of food microbiology, termed predictive microbiology. This concept was introduced and extensively discussed (with particular reference to growth of food-borne pathogens) by McMeekin and his colleagues at the University of Tasmania.[1]

Predictive microbiology has application in both microbial safety and quality of foods; indeed, early development of the concept was based on seafood spoilage. Extensive research in recent years has shown, however, that the most important application of predictive microbiology is in support of food safety initiatives. Microbial growth and survival models are now sufficiently detailed and accurate to make important contributions — scientists and regulators can make reasonable predictions of the relative risk posed by a particular food or food process. It has been argued, however, that predictive microbiology is a misnomer, for predictive microbiology does not actually make predictions at all. To examine this further, we need to first look at some definitions of modeling.

In a general sense, a model simplifies a system by using a combination of descriptions, mathematical functions or equations, and specific starting conditions. There are two general classes of models: descriptive and explanatory, the latter being composed of analytical and numerical models. Descriptive (i.e., observational, empirical, "black box," or inductive) models are data-driven — approaches such as polynomial functions, artificial neural nets, and principal component analysis are used to classify the data. True predictions with this class of models are difficult to make because models cannot be extrapolated beyond the data used to build the

model. In spite of this, descriptive models have been used extensively with considerable success in predictive microbiology.

Explanatory (i.e., mechanistic, "white box," or deductive) models aim to relate the given data to fundamental scientific principles, or at least to measurable physiological processes. Many predictive microbiology models have parameters that are related to observed phenomena and are therefore considered mechanistic. Analytical models — explicit equations that can be fit to data — are the most common form of mechanistic models. To be truly mechanistic, however, a model should raise new questions and hypotheses that can be tested. This is not always easy with explicit functions, however, because it is difficult to extend such functions to dynamic situations or add additional steps to the model. Numerical approaches are designed specifically to allow further development of the model. These models are hierarchical, containing submodels at least one level deeper than the response being described. They have been extensively developed for complex ecological systems, but have not been applied to any great extent in predictive microbiology. Because their use requires extensive programming skills, numerical models have been difficult for nonmathematicians to apply. New software platforms and concepts, such as object-oriented programming, have provided new tools, allowing microbiologists to expand on traditional modeling approaches.

The models discussed so far (and the majority of existing predictive microbiology models) have all been deterministic. In a deterministic model, knowledge of the starting conditions, combined with a mathematical function describing the behavior of the system over time, is sufficient to predict the state of the system at any point in time. Bacteria, however, are not so cooperative. While it may be possible to define a function, the starting conditions are less clear — particularly when dealing with individual bacterial cells. Models that recognize and account for uncertainty or variability in an experimental system are called stochastic or probabilistic models. Probability models have been used extensively in the past to predict the probability of germination of pathogenic spore-forming bacteria. Recently, the behavior of individual bacteria has been likened to that of atoms, in a concept referred to as quantal microbiology, analogous in some ways to quantum mechanics.[2] In addition, the effect of environmental stress on microorganisms leads to interpopulation diversity, where individual cells may be phenotypically but not genetically different from each other.[3] Recent advances in the use of software that allows the development of probability models have helped to make these approaches more accessible and provided more support for the development of risk assessment procedures.

McMeekin's monograph set the stage for an explosive increase in predictive microbiology research in the last decade of the 20th century. As we begin the new millennium, there is a need for a definitive work on the subject, above and beyond the many comprehensive and stimulating reviews that have appeared. This book is intended to serve many purposes. First, we believe it will be a primer for many who are not familiar with the field. Chapter 1, "Experimental Design and Data Collection"; Chapter 2, "Primary Models"; and Chapter 3, "Secondary Models" are designed in part to give the uninitiated sufficient information to start developing their own models. Other chapters address more complex issues such as the difficulties in fitting models (Chapter 4, "Model Fitting and Uncertainty") and the relevance of models to the real

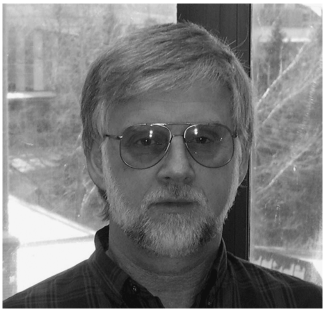
world (Chapter 5, “Challenge of Food and the Environment”). Extensive applications of predictive microbiology are covered in Chapter 6, “Software Programs to Increase the Utility of Predictive Microbiology Information,” and in Chapter 7, “Modeling Microbial Dynamics under Time-Varying Conditions.” The important contribution made by predictive microbiology to quantitative risk assessment is described in Chapter 8, “Predictive Microbiology in Quantitative Risk Assessment”; and the further complication of individual cell behavior and intercell variability is addressed in Chapter 9, “Modeling the History Effect on Microbial Growth and Survival: Deterministic and Stochastic Approaches.” The future of predictive microbiology is the subject of Chapter 10, “Models — What Comes after the Next Generation?” Application of predictive microbiology concepts to the study of fungi is dealt with in Chapter 11, “Predictive Mycology”; and in Chapter 12, “An Essay on the Unrealized Potential of Predictive Microbiology,” Tom McMeekin discusses the contribution made by predictive modeling to the field of food microbiology.

We have attempted to cover the basics of predictive microbiology, as well as the more up-to-date and challenging aspects of the field. There are extensive references to earlier work, as well as to recent publications. It is anticipated that this book will reflect the extensive research that has been instrumental in placing predictive microbiology at the forefront of food microbiology, and that it will stimulate future discussion and research in this exciting field.

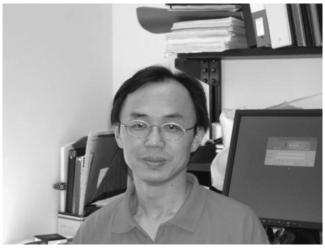
REFERENCES

1. McMeekin, T.A., Olley, J.N., Ross, T., and Ratkowsky, D.A., *Predictive Microbiology: Theory and Application,* John Wiley & Sons, New York, 1993.
2. Bridson, E.Y. and Gould, G.W., Quantal microbiology, *Lett. Appl. Microbiol.,* 30, 95, 2000.
3. Booth, I.R., Stress and the single cell: intrapopulation diversity is a mechanism to ensure survival upon exposure to stress, *Int. J. Food Microbiol.,* 78, 19, 2002.

About the Editors



Robin C. McKellar is a senior research scientist who obtained a B.Sc. in biology and chemistry, an M.Sc. in microbiology from the University of Waterloo, and a Ph.D. in microbiology from the University of Ottawa. Dr. McKellar joined the Food Research Institute in Ottawa in 1979 to study the problem of psychrotrophic bacteria in milk. After the formation of the Centre for Food and Animal Research, he served as team leader of the Food Safety Team and initiated a research program on the control of food-borne pathogens. He relocated to Guelph in 1996, and now serves as program science advisor for Theme 410 (Food Safety), and research leader of the Food Preservation Technologies section at the Food Research Program. He has been actively involved in research in such areas as quality of dairy products; enzymatic and microbiological methods development; characterization of the virulence factors of food-borne pathogens; control of pathogens using antimicrobial agents; use of the electronic nose to monitor quality of foods and beverages; and mathematical modeling of pathogen survival and growth in foods. He is currently an adjunct professor with the Department of Food Science, University of Guelph, and has cosupervised several graduate students.



Xuewen Lu is an assistant professor of statistics in the Department of Mathematics and Statistics at the University of Calgary, Canada. Before he joined the university, he was a research scientist in the Atlantic Food and Horticulture Research Centre, Agriculture and Agri-Food Canada from 1997 to 1998, a biostatistician at the Food Research Program, Agriculture and Agri-Food Canada, and a Special Graduate Faculty member at the University of Guelph from 1998 to 2002. He is a member of the Statistical Society of Canada and the Canadian Research Institute for Food Safety, University of Guelph. His main research areas are functional data analysis, survival analysis, and predictive microbiology. He has cosupervised several graduate students. He received his B.Sc. degree (1987) in mathematics from Hunan Normal University, China, M.Sc. degree (1990) in statistics from Peking University, China, and Ph.D. degree (1997) in statistics from the University of Guelph.

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